

Package ‘ouxy’

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Type Package

Title Model of Adaptive Trait Evolution

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Author Dwueng-Chwuan Jhwueng

Maintainer Dwueng-Chwuan Jhwueng <dc.jhwueng@fcu.edu.tw>

Description Performs statistical inference on the models of adaptive trait evolution under approximate Bayesian computation. This can simulate traits from four models, compute trait data summary statistics. Parameters are estimated under Approximate Bayesian Computation, model selection as well as posterior parameter mean will be reported. Users need to enter a comparative dataset and a phylogenetic tree.

License GPL (>= 2)

RoxygenNote 6.1.1

Depends R (>= 3.5.0)

Imports stats, ape, coda, Sim.DiffProc, MCMCpack, abc, phytools, nlme, TreeSim, adephylo, maps, geiger, EasyABC, utils

Suggests testthat

BugReports <https://github.com/djhwueng/ououcir/issues>

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NeedsCompilation no

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bat

Bat dataset

Description

A dataset containing a phylogenetic tree and trait data for bat species

Usage

`data(bat)`

Format

A list of two items

`tree` the phylogenetic tree object

`traitset` a data frame of trait data

References

Aguirre, Luis F., et al. "Ecomorphological analysis of trophic niche partitioning in a tropical savannah bat community." *Proceedings of the Royal Society of London. Series B: Biological Sciences* 269.1497 (2002): 1271-1278.

coral	<i>Coral dataset</i>
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Description

A dataset containing a phylogenetic tree and trait data for coral species

Usage

```
data(coral)
```

Format

A list of two items

tree the phylogenetic tree object

traitset a data frame of trait data

References

Sanchez, Juan Armando, and Howard R. Lasker. "Patterns of morphological integration in marine modular organisms: supra-module organization in branching octocoral colonies." *Proceedings of the Royal Society of London. Series B: Biological Sciences* 270.1528 (2003): 2039-2044.

HyperParam	<i>The range of parameters</i>
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Description

Set up range for parameters for next step

Usage

```
HyperParam(tree = tree, traitset = traitset)
```

Arguments

tree An ape: tree object stored in phylo format

traitset a dataframe that contains 3 traits

Details

Function [OUprior](#) is called to compute the model estimate, then return the range for parameter estimate for next step analysis. The range is set to 3 times larger/smaller than the parameter estimates. Function [regboundfcn](#) is called to get the bound of regression parameter. The ancestral value (root) is computed for each traits in order to used for simulation in the four functions [oubmbmTrait](#), [ououbmTrait](#), [oubmcirTrait](#) and [ououcirTrait](#).

Value

A list of vectors of sample of model parameters, regression parameter and ancestral values.

Examples

```
## using coral dataset (running time more > 5 sec)

data(coral)
tree<-coral$tree
traitset<-coral$traitset
HyperParam(tree=tree,traitset=traitset)
```

lizard

Lizard dataset

Description

A dataset containing a phylogenetic tree and trait data for lizard species

Usage

```
data(lizard)
```

Format

A list of two items

tree the phylogenetic tree object

traitset a data frame of trait data

References

Molina-Borja, M., & Rodriguez-Dominguez, M. A. (2004). Evolution of biometric and life-history traits in lizards (*Gallotia*) from the Canary Islands. *Journal of Zoological Systematics and Evolutionary Research*, 42(1), 44-53.

 oubmbmodel

 Simulate traits under OUBMBM model given a set of parameters

Description

Simulate traits under OUBMBM model given a set of model parameters, regression parameters, tree and ancestral values.

Usage

```
oubmbmodel(model.params, reg.params, root = root, tree = tree)
```

Arguments

model.params	A vector of model parameters including alpha.y: force parameter of response trait, sigmasq.x: rate parameter of covariate and tau: rate parameter of response trait
reg.params	A vector of regression parameters including b0: intercept parameter of regression, b1: slope parameter of first covariate, b2: slope parameter of the second covariate
root	A vector of numerical values for root of species estimated from OUprior estimated from OUprior
tree	An ape: tree object stored in phylo format

Details

The model requires user to input model parameters $\alpha_y, \sigma_x^2, \tau$ and regression parameters b_0, b_1, b_2 , a tree object, trait dataset (one response, two covariate), ancestral values (root) which is estimated by BM or OU model from [geiger](#). Then the algorithm starts from the root and apply the tree traversal algorithm to simulate trait on each node according the OUOUBM dynamics.

Value

Returns the trait vectors $Y = (y_1, y_2, \dots, y_n)'$, $X_1 = (x_{1,1}, x_{1,2}, \dots, x_{1,n})'$, $X_2 = (x_{2,1}, x_{2,2}, \dots, x_{2,n})'$ simulated from the model.

References

1. Jhwueng, D-C. (2019) Statistical modeling for adaptive trait evolution. Under review.
2. Jhwueng, D-C., and Vasileios Maroulas. "Adaptive trait evolution in random environment." *Journal of Applied Statistics* 43.12 (2016): 2310-2324.
3. Hansen, Thomas F., Jason Pienaar, and Steven Hecht Orzack. "A comparative method for studying adaptation to a randomly evolving environment." *Evolution: International Journal of Organic Evolution* 62.8 (2008): 1965-1977.

Examples

```

library(ape)
tree<-rcoal(5)
tree<-reorder(tree,"postorder")
root<-list(y.ou.sigmsq=1 ,y.ou.root=0, x1.ou.root=0, x2.ou.root=0,x1.bm.root=0, x2.bm.root=0)
model.params<-c(0.5,1,0.2)
names(model.params)<-c("alpha.y","sigmasq.x","tau")
reg.params<-c(0,1,1)
names(reg.params)<-c("b0","b1","b2")
oubmbmmodel(model.params,reg.params,root=root,tree=tree)

```

oubmbmprior

Draw prior samples for OUBMBM model

Description

Simulate sample for parameters in OUBMBM model given a set of hyper parameters

Usage

```

oubmbmprior(prior.model.params = prior.model.params,
            prior.reg.params = prior.reg.params)

```

Arguments

prior.model.params

A vectors of hyper parameters for model parameter containing (alpha.y.min, alpha.y.max) for alpha.y, (sigmasq.x.min, sigmasq.x.max) for sigmasq.x, (tau.y.min, tau.max) for rate parameter of tau

prior.reg.params

A vector of hyper paramter for regression parameters. (b0.min,b0.max) for b0, (b1.min,b1.max) for b1, (b2.min,b2.max) for b2

Details

The function requires user to input hyper parameters for α_y , σ_x^2 , τ and hyper parameters for regression parameters b_0 , b_1 , b_2 from uniform distribution with its minimum and maximum values.

Value

Returns the samples of model parameters and regression parameter

Examples

```
prior.model.params<-c(0,3,0,3,0,1)

names(prior.model.params)<-c("alpha.y.min","alpha.y.max",
"tau.min","tau.max","sigmasq.x.min","sigmasq.x.max")

prior.reg.params<-c(-3, 3, -3, 3, -3, 3)
names(prior.reg.params)<-c("b0.min", "b0.max", "b1.min", "b1.max", "b2.min", "b2.max")
oubmbmprior(prior.model.params=prior.model.params,prior.reg.params=prior.reg.params)
```

oubmbmTrait

Parameter samples and summary statistics

Description

Draw sample for parameters, simulate trait and compute the summary statistics for OUBMBM model

Usage

```
oubmbmTrait(tree = tree, traitset = traitset, sims = sims)
```

Arguments

tree	An ape: tree object stored in phylo format
traitset	a dataframe that contains 3 traits
sims	number of trait replicate

Details

Given tree, trait sets, function [HyperParam](#) is called to yield the range of parameters, then function [oubmbmprior](#) is called to draw sample for parameter, then the function [oubmbmmodel](#) is applied to simulate traits through post order tree traversal algorithm, finally the summary statistics is computed by function [sumstat](#).

Value

A list of vectors containing a dataframe of summary statistics, and a dataframe of parameter samples

Examples

```
## using bat dataset (running time more > 5 sec)

data(bat)
tree<-bat$tree
traitset<-bat$traitset
sims<-10
oubmbmTrait(tree=tree,traitset=traitset,sims=sims)
```

oubmcirmodel

Simulate traits under OUBMCIR model given a set of parameters

Description

Simulate traits under OUBMCIR model given a set of model parameters, regression parameters, tree and ancestral values.

Usage

```
oubmcirmodel(model.params, reg.params, root = root, tree = tree)
```

Arguments

model.params	A vector of model parameters including alpha.y: force parameter of response trait, sigmasq.x: rate parameter of covariate, alpha.tau: force parameter of rate, theta.tau optimum parameter of rate, sigmasq.tau: rate parameter of rate
reg.params	A vector of regression paramters including b0: intercept parameter of regression, b1: slope parameter of first covariate, b2: slope paramter of the second covariate
root	A vector of numerical values for root of species estimated from OUprior
tree	An ape: tree object stored in phylo format

Details

The model requires user to input model parameters $\alpha_y, \sigma_x^2, \alpha_\tau, \theta_\tau, \sigma_\tau^2$ and regression parameters b_0, b_1, b_2 , a tree object, trait dataset (one response, two covariate), ancestral values(root) which is estimated by BM or OU model from [geiger](#). Then the algorithm starts from the root and apply the tree traversal algorithm to simulate trait on each node according the OUOUBM dynamics.

Value

Returns the trait vectors $Y = (y_1, y_2, \dots, y_n)'$, $X_1 = (x_{1,1}, x_{1,2}, \dots, x_{1,n})'$, $X_2 = (x_{2,1}, x_{2,2}, \dots, x_{2,n})'$ simulated from the model.

References

1. Jhwueng, D-C. (2019) Statistical modeling for adaptive trait evolution. Under review.
2. Jhwueng, D-C., and Vasileios Maroulas. "Adaptive trait evolution in random environment." *Journal of Applied Statistics* 43.12 (2016): 2310-2324.
3. Hansen, Thomas F., Jason Pienaar, and Steven Hecht Orzack. "A comparative method for studying adaptation to a randomly evolving environment." *Evolution: International Journal of Organic Evolution* 62.8 (2008): 1965-1977.

Examples

```
library(ape)
tree<-rcoal(5)
tree<-reorder(tree,"postorder")
root<-list(y.ou.sigmsq=1 ,y.ou.root=0, x1.ou.root=0, x2.ou.root=0,x1.bm.root=0, x2.bm.root=0)
model.params<-c(0.5,0.25,0.3,1,0.2)
names(model.params)<-c("alpha.y","alpha.x","theta.x","sigmasq.x","sigmasq.tau")
reg.params<-c(0,1,1)
names(reg.params)<-c("b0","b1","b2")
oubmcirmodel(model.params,reg.params,root=root,tree=tree)
```

oubmcirprior

Draw prior samples for OUBMCIR model

Description

Simulate sample for parameters in OUBMCIR model given a set of hyper parameters

Usage

```
oubmcirprior(prior.model.params = prior.model.params,
             prior.reg.params = prior.reg.params)
```

Arguments

prior.model.params

A vectors of hyper parameters for model parameter containing (alpha.y.min, alpha.y.max) for alpha.y, (sigmasq.x.min, sigmasq.x.max) for sigmasq.x, (alpha.tau.min, alpha.tau.max) for alpha.tau, (theta.tau.min, theta.tau.max) for theta_tau, (sigmasq.tau.min, sigmasq.tau.max) for rate parameter of tau

prior.reg.params

A vector of hyper paramter for regression parameters. (b0.min,b0.max) for b0, (b1.min,b1.max) for b1, (b2.min,b2.max) for b2

Details

The function requires user to input hyper parameters for $\alpha_y, \sigma_x^2, \alpha_\tau, \theta_\tau, \sigma_\tau^2$ and hyper parameters for regression parameters b_0, b_1, b_2 from uniform distribution with its minimum and maximum values.

Value

Returns the samples of model parameters and regression parameter

Examples

```
prior.model.params<-c(0,3,0,3,0,1,0,3,0,2,0,1.5)

names(prior.model.params)<-c(
"alpha.y.min","alpha.y.max","sigmasq.x.min","sigmasq.x.max",
"alpha.tau.min","alpha.tau.max","theta.tau.min","theta.tau.max",
"sigmasq.tau.min","sigmasq.tau.max")
prior.reg.params<-c(-3, 3, -3, 3, -3, 3)
names(prior.reg.params)<-c("b0.min", "b0.max", "b1.min", "b1.max", "b2.min", "b2.max")
oubmcirprior(prior.model.params=prior.model.params,prior.reg.params=prior.reg.params)
```

oubmcirTrait

Parameter samples and summary statistics

Description

Draw sample for parameters, simulate trait and compute the summary statistics for OUBMCIR model

Usage

```
oubmcirTrait(tree = tree, traitset = traitset, sims = sims)
```

Arguments

tree	An ape: tree object stored in phylo format
traitset	a dataframe that contains 3 traits
sims	number of trait replicate

Details

Given tree, trait sets, function [HyperParam](#) is called to yield the range of parameters, then function [oubmbmprior](#) is called to draw sample for parameter, then the function [oubmbmmodel](#) is applied to simulate traits through post order tree traversal algorithm, finally the summary statistics is computed by function [sumstat](#).

Value

A list of vectors containing a dataframe of summary statistics, and a dataframe of parameter samples

Examples

```
## using coral dataset (running time more > 5 sec)

data(coral)
tree<-coral$tree
traitset<-coral$traitset
sims<-10
oumbcirTrait(tree=tree,traitset=traitset,sims=sims)
```

ououbmmodel

Simulate traits under OUOUBM model given a set of parameters

Description

Simulate traits under OUOUBM model given a set of model parameters, regression parameters, tree and ancestral values.

Usage

```
ououbmmodel(model.params, reg.params, root = root, tree = tree)
```

Arguments

model.params	A vector of model parameters including alpha.y: force parameter of response trait, alpha.x: force parameter of covariate, theta.x: optimum parameter of covariate, sigmasq.x: rate parameter of covariate and tau rate parameter of response trait
reg.params	A vector of regression paramters including b0: intercept parameter of regression, b1: slope parameter of first covariate, b2: slope paramter of the second covariate
root	A vector of numerical values for root of species estimated from OUprior
tree	An ape: tree object stored in phylo format

Details

The model requires user to input model parameters $\alpha_y, \alpha_x, \theta_x, \sigma_x^2, \tau$ and regression parameters b_0, b_1, b_2 , a tree object, trait dataset (one response, two covariate), ancestral values(root) which is estimated by BM or OU model from [geiger](#). Then the algorithm starts from the root and apply the tree traversal algorithm to simulate trait on each node according the OUOUBM dynamics.

Value

Returns the trait vectors $Y = (y_1, y_2, \dots, y_n)'$, $X_1 = (x_{1,1}, x_{1,2}, \dots, x_{1,n})'$, $X_2 = (x_{2,1}, x_{2,2}, \dots, x_{2,n})'$ simulated from the model.

References

1. Jhwueng, D-C. (2019) Statistical modeling for adaptive trait evolution. Under review.
2. Jhwueng, D-C., and Vasileios Maroulas. "Adaptive trait evolution in random environment." *Journal of Applied Statistics* 43.12 (2016): 2310-2324.
3. Hansen, Thomas F., Jason Pienaar, and Steven Hecht Orzack. "A comparative method for studying adaptation to a randomly evolving environment." *Evolution: International Journal of Organic Evolution* 62.8 (2008): 1965-1977.

Examples

```
library(ape)
tree<-rcoal(5)
tree<-reorder(tree,"postorder")
root<-list(y.ou.sigmsq=1 ,y.ou.root=0, x1.ou.root=0, x2.ou.root=0,x1.bm.root=0, x2.bm.root=0)
model.params<-c(0.5,0.25,0,1,0.2)
names(model.params)<-c("alpha.y","alpha.x","theta.x","sigmasq.x","tau")
reg.params<-c(0,1,1)
names(reg.params)<-c("b0","b1","b2")
ououbmmodel(model.params,reg.params,root=root,tree=tree)
```

ououbmprior

Draw prior samples for OUOUBM model

Description

Simulate sample for parameters in OUOUBM model given a set of hyper parameters

Usage

```
ououbmprior(prior.model.params = prior.model.params,
            prior.reg.params = prior.reg.params)
```

Arguments

prior.model.params

A vectors of hyper parameters for model parameter containing (alpha.y.min, alpha.y.max) for alpha.y, (alpha.x.min, alpha.x.max) for alpha.x,(theta.y.min, theta.y.max) for theta.y, (sigmasq.x.min, sigmasq.x.max) for sigmasq.x, (tau.y.min, tau.max) for rate parameter of tau

prior.reg.params

A vector of hyper paramter for regression parameters. (b0.min,b0.max) for b0, (b1.min,b1.max) for b1, (b2.min,b2.max) for b2

Details

The function requires user to input hyper parameters for $\alpha_y, \alpha_x, \theta_x, \sigma_x^2, \tau$ and hyper parameters for regression parameters b_0, b_1, b_2 from uniform distribution with its minimum and maximum values.

Value

Returns the samples of model parameters and regression parameter

Examples

```
prior.model.params<-c(0,3,0,3,-5,5,0,1,0,2)
names(prior.model.params)<-c(
"alpha.y.min","alpha.y.max","alpha.x.min","alpha.x.max",
"theta.x.min","theta.x.max","sigmasq.x.min","sigmasq.x.max",
"tau.min","tau.max")
prior.reg.params<-c(-3, 3, -3, 3, -3, 3)
names(prior.reg.params)<-c("b0.min", "b0.max", "b1.min", "b1.max", "b2.min", "b2.max")
ououbmprior(prior.model.params=prior.model.params,prior.reg.params=prior.reg.params)
```

ououbmTrait

Parameter samples and summary statistics

Description

Draw sample for parameters, simulate trait and compute the summary statistics for OUOUBM model

Usage

```
ououbmTrait(tree = tree, traitset = traitset, sims = sims)
```

Arguments

tree	An ape: tree object stored in phylo format
traitset	a dataframe that contains 3 traits
sims	number of trait replicate

Details

Given tree, trait sets, function [HyperParam](#) is called to yield the range of parameters, then function [ououbmprior](#) is called to draw sample for parameter, then the function [ououbmmodel](#) is applied to simulate traits through post order tree traversal algorithm, finally the summary statistics is computed by function [sumstat](#).

Value

A list of vectors containing a dataframe of summary statistics, and a dataframe of parameter samples

Examples

```
## using lizard dataset (running time more > 5 sec)

data(lizard)
tree<-lizard$tree
traitset<-lizard$traitset
sims<-10
ououbmTrait(tree=tree,traitset=traitset,sims=sims)
```

ououcirmodel

Simulate traits under OUBMCIR model given a set of parameters

Description

Simulate traits under OUBMCIR model given a set of model parameters, regression parameters, tree and ancestral values.

Usage

```
ououcirmodel(model.params, reg.params, root = root, tree = tree)
```

Arguments

model.params	A vector of model parameters including alpha.y: force parameter of response trait, alpha.x: force parameter of covariate, theta.x" optimum parameter of covariate, sigmasq.x: rate parameter of covariate, alpha.tau: force parameter of rate, theta.tau optimum parameter of rate, sigmasq.tau: rate parameter of rate
reg.params	A vector of regression paramters including b0: intercept parameter of regression, b1: slope parameter of first covariate, b2: slope paramter of the second covariate
root	A vector of numerical values for root of species estimated from OUprior
tree	An ape: tree object stored in phylo format

Details

The model requires user to input model parameters $\alpha_y, \alpha_x, \theta_x, \sigma_x^2, \alpha_\tau, \theta_\tau, \sigma_\tau^2$ and regression parameters b_0, b_1, b_2 , a tree object, trait dataset (one response, two covariate), ancestral values(root) which is estimated by BM or OU model from [geiger](#). Then the algorithm starts from the root and apply the tree traversal algorithm to simulate trait on each node according the OUOUBM dynamics.

Value

Returns the trait vectors $Y = (y_1, y_2, \dots, y_n)'$, $X_1 = (x_{1,1}, x_{1,2}, \dots, x_{1,n})'$, $X_2 = (x_{2,1}, x_{2,2}, \dots, x_{2,n})'$ simulated from the model.

References

1. Jhwueng, D-C. (2019) Statistical modeling for adaptive trait evolution. Under review.
2. Jhwueng, D-C., and Vasileios Maroulas. "Adaptive trait evolution in random environment." *Journal of Applied Statistics* 43.12 (2016): 2310-2324.
3. Hansen, Thomas F., Jason Pienaar, and Steven Hecht Orzack. "A comparative method for studying adaptation to a randomly evolving environment." *Evolution: International Journal of Organic Evolution* 62.8 (2008): 1965-1977.

Examples

```
library(ape)
tree<-rcoal(5)
tree<-reorder(tree,"postorder")
root<-list(y.ou.sigmsq=1 ,y.ou.root=0, x1.ou.root=0, x2.ou.root=0,x1.bm.root=0, x2.bm.root=0)
model.params<-c(0.5,0.25,0,1,0.125,0.15,0.2)
names(model.params)<-c("alpha.y","alpha.x","theta.x","sigmasq.x"
,"alpha.tau","theta.tau","sigmasq.tau")
reg.params<-c(0,1,1)
names(reg.params)<-c("b0","b1","b2")
ououcirmodel(model.params,reg.params,root=root,tree=tree)
```

ououcirprior

Draw prior samples for OUOUCIR model

Description

Simulate sample for parameters in OUOUCIR model given a set of hyper parameters

Usage

```
ououcirprior(prior.model.params = prior.model.params,
prior.reg.params = prior.reg.params)
```

Arguments

prior.model.params

A vectors of hyper parameters for model parameter containing (alpha.y.min, alpha.y.max) for alpha.y, (alpha.x.min, alpha.x.max) for alpha.x, (theta.x.min, theta.x.max) for theta.x, (sigmasq.x.min, sigmasq.x.max) for sigmasq.x, (alpha.tau.min, alpha.tau.max) for alpha.tau, (theta.tau.min, theta.tau.max) for theta_tau, (sigmasq.tau.min, sigmasq.tau.max) for rate parameter of tau

prior.reg.params

A vector of hyper paramter for regression parameters. (b0.min,b0.max) for b0, (b1.min,b1.max) for b1, (b2.min,b2.max) for b2

Details

The function requires user to input hyper parameters for $\alpha_y, \alpha_x, \theta_x, \sigma_x^2, \alpha_\tau, \theta_\tau, \sigma_\tau^2$ and hyper parameters for regression parameters b_0, b_1, b_2 from uniform distribution with its minimum and maximum values.

Value

Returns the samples of model parameters and regression parameter

Examples

```
prior.model.params<-c(0,3,0,3,-2,2,0,1,0,3,0,2,0,1.5,0,1)

names(prior.model.params)<-c(
  "alpha.y.min","alpha.y.max","alpha.x.min","alpha.x.max",
  "theta.x.min","theta.x.max","sigmasq.x.min","sigmasq.x.max",
  "alpha.tau.min","alpha.tau.max","theta.tau.min","theta.tau.max",
  "sigmasq.tau.min","sigmasq.tau.max")
prior.reg.params<-c(-3, 3, -3, 3, -3, 3)
names(prior.reg.params)<-c("b0.min", "b0.max", "b1.min", "b1.max", "b2.min", "b2.max")
ououcirprior(prior.model.params=prior.model.params,prior.reg.params=prior.reg.params)
```

ououcirTrait

Parameter samples and summary statistics

Description

Draw sample for parameters, simulate trait and compute the summary statistics for OUOUCIR model

Usage

```
ououcirTrait(tree = tree, traitset = traitset, sims = sims)
```


Arguments

tree	An ape: tree object stored in phylo format
traitset	a dataframe that contains 3 traits
sims	number of trait replicate

Details

Given tree, trait sets, function `HyperParam` is called to yield the range of parameters, then function `oubmbmprior` is called to draw sample for parameter, then the function `oubmbmmodel` is applied to simulate traits through post order tree traversal algorithm, finally the summary statistics is computed by function `sumstat`.

Value

A list of vectors containing a dataframe of summary statistics, and a dataframe of parameter samples

Examples

```
## using bat dataset (running time more > 5 sec)

data(bat)
tree<-bat$tree
traitset<-bat$traitset
sims<-10
ououcirTrait(tree=tree,traitset=traitset,sims=sims)
```

OUprior

Fit OU model for univariate data

Description

Fit OU model given tree and trait

Usage

```
OUprior(tree = tree, trait = trait, model = model)
```

Arguments

tree	An ape: tree object stored in phylo format
trait	a univariate trait
model	specified model preset "OU".

Details

Parameter estimates α, θ, σ^2 are estimated by BM (when $\alpha = 0$) or OU model from [geiger](#) for the next step analysis with function `HyperParam` to get the reasonable range of the hyper parameter as well as the ancestral value.

Value

MLE parameter estimates α, θ, σ^2 .

References

1. Jhwueng, D-C. (2019) Statistical modeling for adaptive trait evolution. Under review.
2. Jhwueng, D-C., and Vasileios Maroulas. "Adaptive trait evolution in random environment." *Journal of Applied Statistics* 43.12 (2016): 2310-2324.
3. Hansen, Thomas F., Jason Pienaar, and Steven Hecht Orzack. "A comparative method for studying adaptation to a randomly evolving environment." *Evolution: International Journal of Organic Evolution* 62.8 (2008): 1965-1977.

Examples

```
library(ape)
tree<-rcoal(3)
trait<-rnorm(3)
names(trait)<-tree$tip.label
model <- "OU"
OUprior(tree=tree,trait=trait,model=model)
```

ouxy

main program to perform analysis

Description

Analyze data and report the model estimates and model selection

Usage

```
ouxy(tree = tree, traitset = traitset, tol = 0.1, sims = 100)
```

Arguments

<code>tree</code>	An ape: tree object stored in phylo format
<code>traitset</code>	a dataframe that contains 3 traits
<code>tol</code>	acceptance rate from ABC
<code>sims</code>	number of trait replicate

Details

`ouxy` performs data analysis under Approximate Bayesian Computation(ABC) procedure. The summary statistics for the raw traitsets are first computed by by function `sumstat`, and the parameters ranges are computed using the tree and traitsets under function `HyperParam`, and sample of prior paramters are drawn from function `oubmbmprior`, then the function `oubmbmmodel` is applied to simulate traits through post order tree traversal algorithm. The ABC procedure are then performed using sample of paramters and simulated traitset. Posterior sample are chosen using acceptance rate $\text{sims} * \text{tol}$. The posterior samples are computed using rejection method `abc` to median of the posterior samples are as reported parameter estimate and Bayes factor is computed using function `postpr` accordingly by the ratio of the posterior model probability under each model.

Value

A list of vectors containing a dataframe of model parameter estimate, and a dataframe of Bayes factors between a pair of models

1. **table.output**: The posterior median for parameter estimates under each model.
2. **s.mnlog**: Bayes factor tables comparing a pair of models.

Examples

```
## using coral dataset (It takes for a whiles)

data(coral)
tree<-coral$tree
traitset<-coral$traitset
sims<-1000
output<-ouxy(tree=tree,traitset=traitset,tol=0.1,sims= sims)

## OUTPUT THE FOLLOWING
## >output$s.mnlog

## $mnlogistic
## $mnlogistic$Prob
## oubmbm oubmcir ououbm ououcir
## 0.03081341 0.01533086 0.40779579 0.54605995

## $mnlogistic$BayesF
## oubmbm oubmcir ououbm ououcir
## oubmbm 1.00000000 2.00989403 0.07556087 0.05642861
## oubmcir 0.49753867 1.00000000 0.03759446 0.02807542
## ououbm 13.23436292 26.59966708 1.00000000 0.74679673
## ououcir 17.72150620 35.61834960 1.33905246 1.00000000
##
## > output$table.out
## alpha.y alpha.x alpha.tau theta.x theta.tau sigma.x
## OUBMBM 4.3064 NA NA NA NA 7.821074
## OUOUBM 4.1240 5.2119 NA -0.5759 NA 10.117253
## OUBMCIR 4.3720 NA 4.0736 NA 1.2326 7.825912
## OUOUCIR 3.1016 4.4269 3.9930 0.0668 1.2702 9.226803
```

```
## GLS      NA      NA      NA      NA      NA      NA
##
##      tau sigma.tau      b0      b1      b2
## OUBMBM  2.2403      NA 0.1678000 0.03850000 0.2874000
## OUOUBM  2.5021      NA 0.1651000 0.03260000 0.3146000
## OUBMCIR  NA  1.492548 0.1706000 0.03760000 0.3049000
## OUOUCIR  NA  1.516047 0.1661000 0.03480000 0.2549000
## GLS      NA      NA 0.1682413 0.03931911 0.3564761
```

```
regboundfcn      range for regression parameters
```

Description

Set up range for regression parameters

Usage

```
regboundfcn(olssum = olssum)
```

Arguments

olssum summary statistics from ordinary least square performed by [lm](#).

Details

An ordinary least square analysis is performed on regression $y \sim x_1 + x_2$. Parameter estimates \hat{b} and standard errors $sd(\hat{b})$ are used to construct the bound using formula $\hat{b} \pm 3sd(\hat{b})$.

Value

A vectors of values containing the range of regression parameters

Examples

```
resptrait<-rnorm(10)
predtrait1<-rnorm(10)
predtrait2<-rnorm(10)
olssum <- base::summary(lm(resptrait~predtrait1+predtrait2))
regboundfcn(olssum=olssum)
```

sumstat	<i>Summary statistics</i>
---------	---------------------------

Description

Calculate summary statistics given trait and tree

Usage

```
sumstat(trait = trait, tree = tree, ...)
```

Arguments

trait	A vector of numerical trait value
tree	An ape: tree object stored in phylo format
...	relevant argument

Details

This function computes the 12 summary statistics using the trait and tree. [ape](#) is used for computing the contrast trait from the difference between the species and its closet neighbor. For Bloomberg K and Pagel Lambda, statistics are computed using [phytools](#).

Value

Twelve summary statistics: mean, sd, median, skewness, kurtosis from the raw data as well as from data with the difference between two closet neighbors, Bloomberg K and Pagel's lambda.

References

1. Paradis E. & Schliep K. 2018. *ape* 5.0: an environment for modern phylogenetics and evolutionary analyses in R. *Bioinformatics* 35: 526-528.
2. Blomberg, Simon P., Theodore Garland Jr, and Anthony R. Ives. "Testing for phylogenetic signal in comparative data: behavioral traits are more labile." *Evolution* 57.4 (2003): 717-745.
3. Pagel, Mark. "Inferring the historical patterns of biological evolution." *Nature* 401.6756 (1999): 877.
4. Revell, Liam J. "phytools: an R package for phylogenetic comparative biology (and other things)." *Methods in Ecology and Evolution* 3.2 (2012): 217-223.

Examples

```
library(ape)
tree<-rcoal(5)
trait <- rnorm(5)
names(trait)<-tree$tip.label
sumstat(trait=trait,tree=tree)
```


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